

SEQUENCE LISTING

<110> Bledsoe, Randy, K

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<120> STRUCTURE OF A GLUCOCORTICOID RECEPTOR LIGAND BINDING DOMAIN
COMPRISING AND EXPANDED BINDING POCKET AND METHODS EMPLOYING SAME

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<170> PatentIn version 3.1

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30	tat	gga	gtc	tta	act	tgt	gga	agc	tgt	aaa	gtt	ttc	ttc	aaa	aga	gca	1344
	Tyr	Gly	Val	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	
			435					440					445				
	gtg	gaa	gga	cag	cac	aat	tac	cta	tgt	gct	gga	agg	aat	gat	tgc	atc	1392
	Val	Glu	Gly	Gln	His	Asn	Tyr	Leu	Cys	Ala	Gly	Arg	Asn	Asp	Cys	Ile	
		450					455					460					
35	atc	gat	aaa	att	cga	aga	aaa	aac	tgc	cca	gca	tgc	cgc	tat	cga	aaa	1440
	Ile	Asp	Lys	Ile	Arg	Arg	Lys	Asn	Cys	Pro	Ala	Cys	Arg	Tyr	Arg	Lys	
	465					470					475					480	
40	tgt	ctt	cag	gct	gga	atg	aac	ctg	gaa	gct	cga	aaa	aca	aag	aaa	aaa	1488
	Cys	Leu	Gln	Ala	Gly	Met	Asn	Leu	Glu	Ala	Arg	Lys	Thr	Lys	Lys	Lys	
					485					490					495		
45	ata	aaa	gga	att	cag	cag	gcc	act	aca	gga	gtc	tca	caa	gaa	acc	tct	1536
	Ile	Lys	Gly	Ile	Gln	Gln	Ala	Thr	Thr	Gly	Val	Ser	Gln	Glu	Thr	Ser	
				500				505						510			
50	gaa	aat	cct	ggt	aac	aaa	aca	ata	gtt	cct	gca	acg	tta	cca	caa	ctc	1584
	Glu	Asn	Pro	Gly	Asn	Lys	Thr	Ile	Val	Pro	Ala	Thr	Leu	Pro	Gln	Leu	
			515					520					525				
	acc	cct	acc	ctg	gtg	tca	ctg	ttg	gag	gtt	att	gaa	cct	gaa	gtg	tta	1632
	Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu	Glu	Val	Ile	Glu	Pro	Glu	Val	Leu	
		530					535					540					
55	tat	gca	gga	tat	gat	agc	tct	gtt	cca	gac	tca	act	tgg	agg	atc	atg	1680
	Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met	
	545					550				555						560	
60	act	acg	ctc	aac	atg	tta	gga	ggg	cgg	caa	gtg	att	gca	gca	gtg	aaa	1728
	Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	Arg	Gln	Val	Ile	Ala	Ala	Val	Lys	
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	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Arg	Asn	Leu	His	Leu	Asp	Asp	Gln	
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	Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp	Met	Ser	Leu	Met	Ala	Phe	Ala	Leu	
	595						600				605						
10	ggg	tgg	aga	tca	tat	aga	caa	tca	agt	gca	aac	ctg	ctg	tgt	ttt	gct	1872
	Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala	
	610						615				620						
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	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln	Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr	
	625			630						635				640			
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	Asp	Gln	Cys	Lys	His	Met	Leu	Tyr	Val	Ser	Ser	Glu	Leu	His	Arg	Leu	
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25	cag	gta	tct	tat	gaa	gag	tat	ctc	tgt	atg	aaa	acc	tta	ctg	ctt	ctc	2016
	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu	Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu	
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30	tct	tca	gtt	cct	aag	gac	ggc	ctg	aag	agc	caa	gag	cta	ttt	gat	gaa	2064
	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu	Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	
	675						680				685						
35	att	aga	atg	acc	tac	atc	aaa	gag	cta	gga	aaa	gcc	att	gtc	aag	agg	2112
	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu	Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg	
	690						695				700						
40	gaa	gga	aac	tcc	agc	cag	aac	tgg	cag	cgg	ttt	tat	caa	ctg	aca	aaa	2160
	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp	Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	
	705			710						715				720			
45	ctc	ttg	gat	tct	atg	cat	gaa	gtg	gtt	gaa	aat	ctc	ctt	aac	tat	tgc	2208
	Leu	Leu	Asp	Ser	Met	His	Glu	Val	Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys	
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50	ttc	caa	aca	ttt	ttg	gat	aag	acc	atg	agt	att	gaa	ttc	ccc	gag	atg	2256
	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr	Met	Ser	Ile	Glu	Phe	Pro	Glu	Met	
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55	tta	gct	gaa	atc	atc	acc	aat	cag	ata	cca	aaa	tat	tca	aat	gga	aat	2304
	Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln	Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn	
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60	atc	aaa	aaa	ctt	ctg	ttt	cat	caa	aag	tga							2334
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70	<211>	777															
75	<212>	PRT															
80	<213>	Homo sapiens															

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15	Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu	35 40 45
20	Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp	50 55 60
25	Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys	65 70 75 80
30	Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys	85 90 95
35	Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu	100 105 110
40	Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn	115 120 125
45	Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser	130 135 140
50	Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His	145 150 155 160
55	Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr	165 170 175
60	Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp	180 185 190
	Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr	195 200 205
	Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu	210 215 220
	Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn	225 230 235 240

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5	Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys	245	250	255
10	Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr	260	265	270
15	Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr	275	280	285
20	Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala	290	295	300
25	Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser	305	310	315
30	Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met	325	330	335
35	Asn Thr Ala Ser Leu Ser Gln Gln Gln Asp Gln Lys Pro Ile Phe Asn	340	345	350
40	Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln	355	360	365
45	Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro	370	375	380
50	Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro	385	390	395
55	Asp Val Ser Ser Pro Pro Ser Ser Ser Ser Thr Ala Thr Thr Gly Pro	405	410	415
60	Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His	420	425	430
	Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala	435	440	445
	Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile	450	455	460
	Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys	465	470	475
	Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys	485	490	495

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			515					520					525			
10	Thr	Pro	Thr	Leu	Val	Ser	Leu	Leu	Glu	Val	Ile	Glu	Pro	Glu	Val	Leu
		530					535					540				
15	Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met
	545					550					555					560
20	Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	Arg	Gln	Val	Ile	Ala	Ala	Val	Lys
				565						570					575	
25	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	Arg	Asn	Leu	His	Leu	Asp	Asp	Gln
			580						585					590		
30	Met	Thr	Leu	Leu	Gln	Tyr	Ser	Trp	Met	Ser	Leu	Met	Ala	Phe	Ala	Leu
			595					600					605			
35	Gly	Trp	Arg	Ser	Tyr	Arg	Gln	Ser	Ser	Ala	Asn	Leu	Leu	Cys	Phe	Ala
		610					615					620				
40	Pro	Asp	Leu	Ile	Ile	Asn	Glu	Gln	Arg	Met	Thr	Leu	Pro	Cys	Met	Tyr
	625					630					635					640
45	Asp	Gln	Cys	Lys	His	Met	Leu	Tyr	Val	Ser	Ser	Glu	Leu	His	Arg	Leu
					645					650					655	
50	Gln	Val	Ser	Tyr	Glu	Glu	Tyr	Leu	Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu
			660						665					670		
55	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu	Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu
			675					680					685			
60	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu	Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg
		690					695					700				
65	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp	Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys
	705					710					715					720
70	Leu	Leu	Asp	Ser	Met	His	Glu	Val	Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys
					725					730					735	
75	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr	Met	Ser	Ile	Glu	Phe	Pro	Glu	Met
				740					745					750		

Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
755 760 765

5 Ile Lys Lys Leu Leu Phe His Gln Lys
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35 gag gtt att gaa cct gaa gtg tta tat gca gga tat gat agc tct gtt 96
Glu Val Ile Glu Pro Glu Val Leu Tyr Ala Gly Tyr Asp Ser Ser Val
20 25 30

40 cca gac tca act tgg agg atc atg act acg ctc aac atg tta gga ggg 144
Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
35 40 45

45 cgg caa gtg att gca gca gtg aaa tgg gca aag gca ata cca ggt ttc 192
Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
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50 agg aac tta cac ctg gat gac caa atg acc cta ctg cag tac tcc tgg 240
Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
65 70 75 80

atg ttt ctt atg gca ttt gct ctg ggg tgg aga tca tat aga caa tca 288
Met Phe Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
85 90 95

55 agt gca aac ctg ctg tgt ttt gct cct gat ctg att att aat gag cag 336
Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
100 105 110

60 aga atg act cta ccc tgc atg tac gac caa tgt aaa cac atg ctg tat 384
Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
115 120 125

gtt tcc tct gag tta cac agg ctt cag gta tct tat gaa gag tat ctc 432

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	130						135					140					
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	Cys	Met	Lys	Thr	Leu	Leu	Leu	Leu	Ser	Ser	Val	Pro	Lys	Asp	Gly	Leu	
	145					150					155					160	
10	aag	agc	caa	gag	cta	ttt	gat	gaa	att	aga	atg	acc	tac	atc	aaa	gag	528
	Lys	Ser	Gln	Glu	Leu	Phe	Asp	Glu	Ile	Arg	Met	Thr	Tyr	Ile	Lys	Glu	
					165					170					175		
15	cta	gga	aaa	gcc	att	gtc	aag	agg	gaa	gga	aac	tcc	agc	cag	aac	tgg	576
	Leu	Gly	Lys	Ala	Ile	Val	Lys	Arg	Glu	Gly	Asn	Ser	Ser	Gln	Asn	Trp	
				180					185					190			
	cag	cgg	ttt	tat	caa	ctg	aca	aaa	ctc	ttg	gat	tct	atg	cat	gaa	gtg	624
	Gln	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Met	His	Glu	Val	
			195					200					205				
20	gtt	gaa	aat	ctc	ctt	aac	tat	tgc	ttc	caa	aca	ttt	ttg	gat	aag	acc	672
	Val	Glu	Asn	Leu	Leu	Asn	Tyr	Cys	Phe	Gln	Thr	Phe	Leu	Asp	Lys	Thr	
	210						215					220					
25	atg	agt	att	gaa	ttc	ccc	gag	atg	tta	gct	gaa	atc	atc	acc	aat	cag	720
	Met	Ser	Ile	Glu	Phe	Pro	Glu	Met	Leu	Ala	Glu	Ile	Ile	Thr	Asn	Gln	
	225					230					235					240	
30	ata	cca	aaa	tat	tca	aat	gga	aat	atc	aaa	aaa	ctt	ctg	ttt	cat	caa	768
	Ile	Pro	Lys	Tyr	Ser	Asn	Gly	Asn	Ile	Lys	Lys	Leu	Leu	Phe	His	Gln	
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	Lys																
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	1				5					10					15		
50	Glu	Val	Ile	Glu	Pro	Glu	Val	Leu	Tyr	Ala	Gly	Tyr	Asp	Ser	Ser	Val	
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55	Pro	Asp	Ser	Thr	Trp	Arg	Ile	Met	Thr	Thr	Leu	Asn	Met	Leu	Gly	Gly	
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60	Arg	Gln	Val	Ile	Ala	Ala	Val	Lys	Trp	Ala	Lys	Ala	Ile	Pro	Gly	Phe	
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 20 cca gac tca act tgg agg atc atg act acg ctc aac atg tta gga ggg 144
 Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly
 35 40 45
 25 cgG caa gtg att gca gca gtg aaa tgg gca aag gca ata cca ggt ttc 192
 Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe
 50 55 60
 30 agg aac tta cac ctg gat gac caa atg acc cta ctg cag tac tcc tgg 240
 Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp
 65 70 75 80
 35 atg tcc ctt atg gca ttt gct ctg ggg tgg aga tca tat aga caa tca 288
 Met Ser Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser
 85 90 95
 40 agt gca aac ctg ctg tgt ttt gct cct gat ctg att att aat gag cag 336
 Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln
 100 105 110
 45 aga atg act cta ccc tgc atg tac gac caa tgt aaa cac atg ctg tat 384
 Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr
 115 120 125
 50 gtt tcc tct gag tta cac agg ctt cag gta tct tat gaa gag tat ctc 432
 Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu
 130 135 140
 55 tgt atg aaa acc tta ctg ctt ctc tct tca gtt cct aag gac ggt ctg 480
 Cys Met Lys Thr Leu Leu Leu Leu Ser Ser Val Pro Lys Asp Gly Leu
 145 150 155 160
 60 aag agc caa gag cta ttt gat gaa att aga atg acc tac atc aaa gag 528
 Lys Ser Gln Glu Leu Phe Asp Glu Ile Arg Met Thr Tyr Ile Lys Glu
 165 170 175
 65 cta gga aaa gcc att gtc aag agg gaa gga aac tcc agc cag aac tgg 576
 Leu Gly Lys Ala Ile Val Lys Arg Glu Gly Asn Ser Ser Gln Asn Trp
 180 185 190
 70 cag cgG ttt tat caa ctg aca aaa ctc ttg gat tct atg cat gaa gtg 624
 Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Met His Glu Val
 195 200 205

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	gtt gaa aat ctc ctt aac tat tgc ttc caa aca ttt ttg gat aag acc	672
	Val Glu Asn Leu Leu Asn Tyr Cys Phe Gln Thr Phe Leu Asp Lys Thr	
	210 215 220	
5	atg agt att gaa ttc ccc gag atg tta gct gaa atc atc acc aat cag	720
	Met Ser Ile Glu Phe Pro Glu Met Leu Ala Glu Ile Ile Thr Asn Gln	
	225 230 235 240	
10	ata cca aaa tat tca aat gga aat atc aaa aaa ctt ctg ttt cat caa	768
	Ile Pro Lys Tyr Ser Asn Gly Asn Ile Lys Lys Leu Leu Phe His Gln	
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40	Pro Asp Ser Thr Trp Arg Ile Met Thr Thr Leu Asn Met Leu Gly Gly	
	35 40 45	
45	Arg Gln Val Ile Ala Ala Val Lys Trp Ala Lys Ala Ile Pro Gly Phe	
	50 55 60	
50	Arg Asn Leu His Leu Asp Asp Gln Met Thr Leu Leu Gln Tyr Ser Trp	
	65 70 75 80	
55	Met Ser Leu Met Ala Phe Ala Leu Gly Trp Arg Ser Tyr Arg Gln Ser	
	85 90 95	
60	Ser Ala Asn Leu Leu Cys Phe Ala Pro Asp Leu Ile Ile Asn Glu Gln	
	100 105 110	
60	Arg Met Thr Leu Pro Cys Met Tyr Asp Gln Cys Lys His Met Leu Tyr	
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	Val Ser Ser Glu Leu His Arg Leu Gln Val Ser Tyr Glu Glu Tyr Leu	

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 5 <223> X is any amino acid

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 1 5

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 1 5
 30